



OIEP

## RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/10/084,546

TIME: 10:25:18

Input Set : N:\Crf3\RULE60\10084546.raw

Output Set: N:\CRF3\03132002\J084546.raw

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1 <110> APPLICANT: Cahoon, Rebecca E.
2 <120> TITLE OF INVENTION: Vitamin B Metabolism Proteins
3 <130> FILE REFERENCE: BB-1201-A
4 <140> CURRENT APPLICATION NUMBER: 10/084,546
5 <141> CURRENT FILING DATE: 2002-02-25
6 <150> PRIOR APPLICATION NUMBER: 09/370,295
7 <151> PRIOR FILING DATE: 1999-08-09
8 <160> NUMBER OF SEQ ID NOS: 8
9 <170> SOFTWARE: Microsoft Office 97
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1274
13 <212> TYPE: DNA
14 <213> ORGANISM: Zea mays
15 <400> SEQUENCE: 1
16      gcacgagcac ctctgagcct caagccctca acctccctct tcggcgcgta acgtcagtc 60
17      tcaggtattg gcagcataaa gtgttagatt tgtccttgat tgaggtagcc ctcaaaagg 120
18      caagatgttg tggcgcgcag tacgcagtat ggatgtaata atgcattctt cgagtttcct 180
19      tcttccgaaa ctgtatcaac ctgtcaacaa accagtcaag aactatgctt tagttgttct 240
20      aaaccagcat cttccacgat tcatgcctcg actctgggat catgcaaaact tgaggatctg 300
21      cgctgatgga ggagctaata atatttttga tgagatgtat cagataacca atgatgaaga 360
22      caaaaaaagc accagaaata agtatgttcc agaaataatt gaaggggaca tggattctat 420
23      aagacctgaa gtaaaaactgt tctactctag tcagggatcc aaaatttctg ataagtcaca 480
24      taaccaggag acaacagatc tacacaaatg tatttctcga atccatcatt gtacgcctga 540
25      tgatgaaaaa ccaaactctt gtgtacttgt tactggagca ctagggtgaa ggtttgatca 600
26      cgaggcggca aatatcaatg ttctgtatct gtttccggac atgaggattg tcctcctatc 660
27      agacgattgc ttgatccgac ttcttccgag aacacatcgc catgagcttt atattgagtc 720
28      gtctgttgaa ggaccccatg gtgggctttt cctgtttgga gcaccatcaa caagcacaac 780
29      aactactggc ctgaaatgga atctaagtga atcaaagatg agatttgga gcatgataag 840
30      cacatccaac attgtgcagt cggagaaagt aactgtagaa tctgatgcag atctcttggt 900
31      gacaatttct ctgcgaaatc tgacataagc agttcctagt ttgttatctt ttttcttctc 960
32      tttctgtca agtggaacc aagctcttgt acagccactt ttgtgtttat gagttgtgtg 1020
33      tctggtaaat aaataccatc tgatgacaaa tcgatgaggt ctcatcatta gacaggatgt 1080
34      ctaccacgat cttgaactgc tgatgaatta tgtgaataac acgagcaggc atgatgggtg 1140
35      tatctctctc agttgtataa ctgtattgtt gtacttgcaa cggggtttct tgtataaaat 1200
36      tgttctcaac agttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaataaaa 1260
37      aaaaaaaaaa aaaa 1274
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 267
41 <212> TYPE: PRT
42 <213> ORGANISM: Zea mays
43 <400> SEQUENCE: 2
44      Met Leu Trp Arg Ala Val Arg Ser Met Asp Val Ile Met His Ser Ser
45      1                      5                      10                      15

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46 Ser Phe Leu Leu Pro Lys Leu Tyr Gln Pro Val Asn Lys Pro Val Lys
47                20                25                30
48 Asn Tyr Ala Leu Val Val Leu Asn Gln His Leu Pro Arg Phe Met Pro
49                35                40                45
50 Arg Leu Trp Asp His Ala Asn Leu Arg Ile Cys Ala Asp Gly Gly Ala
51                50                55                60
52 Asn His Ile Phe Asp Glu Met Tyr Gln Ile Thr Asn Asp Glu Asp Lys
53                65                70                75                80
54 Lys Ser Thr Arg Asn Lys Tyr Val Pro Glu Ile Ile Glu Gly Asp Met
55                85                90                95
56 Asp Ser Ile Arg Pro Glu Val Lys Leu Phe Tyr Ser Ser Gln Gly Ser
57                100               105               110
58 Lys Ile Ser Asp Lys Ser His Asn Gln Glu Thr Thr Asp Leu His Lys
59                115               120               125
60 Cys Ile Ser Arg Ile His His Cys Thr Pro Asp Asp Glu Lys Pro Asn
61                130               135               140
62 Leu Cys Val Leu Val Thr Gly Ala Leu Gly Gly Arg Phe Asp His Glu
63                145               150               155               160
64 Ala Ala Asn Ile Asn Val Leu Tyr Leu Phe Ser Asp Met Arg Ile Val
65                165               170               175
66 Leu Leu Ser Asp Asp Cys Leu Ile Arg Leu Leu Pro Arg Thr His Arg
67                180               185               190
68 His Glu Leu Tyr Ile Glu Ser Ser Val Glu Gly Pro His Cys Gly Leu
69                195               200               205
70 Phe Pro Val Gly Ala Pro Ser Thr Ser Thr Thr Thr Gly Leu Lys
71                210               215               220
72 Trp Asn Leu Ser Glu Ser Lys Met Arg Phe Gly Ser Met Ile Ser Thr
73                225               230               235               240
74 Ser Asn Ile Val Gln Ser Glu Lys Val Thr Val Glu Ser Asp Ala Asp
75                245               250               255
76 Leu Leu Trp Thr Ile Ser Leu Arg Asn Leu Thr
77                260               265
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80 <211> LENGTH: 545
81 <212> TYPE: DNA
82 <213> ORGANISM: Zea mays
83 <400> SEQUENCE: 3
84 gctttttcaag catcaagatc atcctcctat cagacgactg ttcaatcttt ctgctcccta 60
85 agacacactc ccacgagatc catattaaga aatcgggtga aggtcctcac tgtggtttga 120
86 ttccgatggg tggaccgtca gctaccacaa caaccacagg gctccgatgg aatttagata 180
87 acaccaacat gatgtatggt ggattgataa gcacatctaa catcgtggat gacgataaag 240
88 taacgggtgac ttcagattct gatctggttt ggaccatata gcttcggaat tgagttcaac 300
89 ttgtataatt ccatgcccaa attttgtcgc ctcaaattac atgtattcag ttcaatatt 360
90 attctgtaac tgggtgtgata ttgttttccg ctgcatgtcg ttatgtccat atatgtgaac 420
91 ttattcttca tagtttagga atccagcatc tgccagccaa atgtcccccac aatctatatt 480
92 cagctgtttc acactttcac tgtttgtgca tctgaatatc aatcaacttt gtcgaaaaaa 540
93 aaaaaa 545
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 96

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97 &lt;212&gt; TYPE: PRT

98 &lt;213&gt; ORGANISM: Zea mays

99 &lt;400&gt; SEQUENCE: 4

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100   Phe Ser Ser Ile Lys Ile Ile Leu Leu Ser Asp Asp Cys Ser Ile Phe
101       1           5           10           15
102   Leu Leu Pro Lys Thr His Ser His Glu Ile His Ile Lys Lys Ser Val
103           20           25           30
104   Glu Gly Pro His Cys Gly Leu Ile Pro Met Gly Gly Pro Ser Ala Thr
105           35           40           45
106   Thr Thr Thr Thr Gly Leu Arg Trp Asn Leu Asp Asn Thr Asn Met Met
107       50           55           60
108   Tyr Gly Gly Leu Ile Ser Thr Ser Asn Ile Val Asp Asp Asp Lys Val
109       65           70           75           80
110   Thr Val Thr Ser Asp Ser Asp Leu Val Trp Thr Ile Ser Leu Arg Asn
111           85           90           95

```

113 &lt;210&gt; SEQ ID NO: 5

114 &lt;211&gt; LENGTH: 945

115 &lt;212&gt; TYPE: DNA

116 &lt;213&gt; ORGANISM: Glycine max

117 &lt;400&gt; SEQUENCE: 5

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118   atgcctttcg catatctcaa cctcaaaactg ccacacaaca ccgctcaact tatctccaag 60
119   cctttactcc acaaagttca actgtgcaac cgcgctcctg agaaacaatc tgaattcctt 120
120   ccatttatca ttgaggacca cgtcgttgga ttcattcaca aggggtttgt tgagcatttg 180
121   agaggctttg ggaatgtgtt cattttcccc aaagataaat ataatggagg cttctacgga 240
122   gactttgttt ctttgcatcc aatgctaaag acagctgagg aaagaaccag tgcagttgga 300
123   tatgtagtag aacgtttggg agaggagcat attccaggga tacggaatga gctttaccct 360
124   gtgatatcat catttggtgc acagattttc ttttcattag aacgtgctgc agctccttat 420
125   tttggcataa aggttttatgg aaccagatg aatggctgtg ttgagctgga tgggcagaag 480
126   cacttatgga tagggaagag aagtgttaca aaatccacat atcctggaat gcttgatgag 540
127   ctagttgcag gaggactgcc gcatggaatc aattgtcagc agaatcttgc aaaggaatgt 600
128   gaagaggaag caggaatacc tagatctatc tctgtcaacg ccataaccggt tgggtgctgtt 660
129   tcatacaaag acattgatgg atatagatac aagagagatg ttctgttctg ttatgatcta 720
130   aaactttcaa aagatttcat tccgaaaaat aaagatggag aagttgatag cttcaagttg 780
131   atccctgtta cacaagttgc agaaatcata cgcaagacac agtttttcaa ggcaaattgc 840
132   gctcttgtaa tcattgattt cctgtttcga catggatata tcactcctga atatgatgga 900
133   tatttggaatc tcctacgaag cttaagaata ggagattgct cctga 945

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135 &lt;210&gt; SEQ ID NO: 6

136 &lt;211&gt; LENGTH: 314

137 &lt;212&gt; TYPE: PRT

138 &lt;213&gt; ORGANISM: Glycine max

139 &lt;400&gt; SEQUENCE: 6

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140   Met Pro Phe Ala Tyr Leu Asn Leu Lys Leu Pro His Asn Thr Ala Gln
141       1           5           10           15
142   Leu Ile Ser Lys Pro Leu Leu His Lys Val Gln Leu Cys Asn Arg Ala
143           20           25           30
144   Pro Glu Lys Gln Ser Glu Phe Leu Pro Phe Ile Ile Glu Asp His Val
145           35           40           45
146   Val Gly Phe Ile His Lys Gly Phe Val Glu His Leu Arg Gly Phe Gly
147       50           55           60

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148 Asn Val Phe Ile Phe Pro Lys Asp Lys Tyr Asn Gly Gly Phe Tyr Gly
149 65 70 75 80
150 Asp Phe Val Ser Leu His Pro Met Leu Lys Thr Ala Glu Glu Arg Thr
151 85 90 95
152 Ser Ala Val Gly Tyr Val Val Glu Arg Leu Gly Glu Glu His Ile Pro
153 100 105 110
154 Gly Ile Arg Asn Glu Leu Tyr Pro Val Ile Ser Ser Phe Gly Ala Gln
155 115 120 125
156 Ile Phe Phe Ser Leu Glu Arg Ala Ala Ala Pro Tyr Phe Gly Ile Lys
157 130 135 140
158 Val Tyr Gly Thr Gln Met Asn Gly Cys Val Glu Leu Asp Gly Gln Lys
159 145 150 155 160
160 His Leu Trp Ile Gly Lys Arg Ser Gly Thr Lys Ser Thr Tyr Pro Gly
161 165 170 175
162 Met Leu Asp Glu Leu Val Ala Gly Gly Leu Pro His Gly Ile Asn Cys
163 180 185 190
164 Gln Gln Asn Leu Ala Lys Glu Cys Glu Glu Glu Ala Gly Ile Pro Arg
165 195 200 205
166 Ser Ile Ser Val Asn Ala Ile Pro Val Gly Ala Val Ser Tyr Lys Asp
167 210 215 220
168 Ile Asp Gly Tyr Arg Tyr Lys Arg Asp Val Leu Phe Cys Tyr Asp Leu
169 225 230 235 240
170 Lys Leu Pro Lys Asp Phe Ile Pro Lys Asn Lys Asp Gly Glu Val Asp
171 245 250 255
172 Ser Phe Lys Leu Ile Pro Val Thr Gln Val Ala Glu Ile Ile Arg Lys
173 260 265 270
174 Thr Gln Phe Phe Lys Ala Asn Cys Ala Leu Val Ile Ile Asp Phe Leu
175 275 280 285
176 Phe Arg His Gly Tyr Ile Thr Pro Glu Tyr Asp Gly Tyr Leu Asp Leu
177 290 295 300
178 Leu Arg Ser Leu Arg Ile Gly Asp Cys Ser
179 305 310
181 <210> SEQ ID NO: 7
182 <211> LENGTH: 1406
183 <212> TYPE: DNA
184 <213> ORGANISM: Glycine max
185 <400> SEQUENCE: 7
186 gcacgagaga aacatctcgt gtcaaaagaa gcatctcgtg tatcgtctcc taaaaaaaaat 60
187 ggaattgatg tgtcattggt cgagctttct tcttcgccg gagaatccta acacgacgtg 120
188 ttcgctttct cttaaagtacg ctctcgttgt tctcaaccaa agcctcccga gatttgctcc 180
189 cctgctttgg gaccacgctc aagtgcgagt ttgtgctgat ggaggtgcca atagggtgta 240
190 tgatgaaatg cctcttttct tccctcatca acaaccttcc catgttcgca ccaggtaaa 300
191 gcctgatgta attaaagggg acatggattc aatcaggaca gaagtacttg acttctatgc 360
192 aaagctggga actaagataa ttgatgagtc tcatgatcag gacaccacag atttacacaa 420
193 atgtgtggca tacatacgtg acctaccccc aaatattgat ggagcagaac tatgcattct 480
194 tgttgctgga gcacttggtg ggagatttga ccatgagatt ggaaatatta acgtgctgtg 540
195 ccgattttcc aacacacgaa ttatccttct atctgatgat tgccctattc accttcttcc 600
196 aaagaatcat tgtcataaaa tctttgttca atcttctgtt gaggggtccgc attgtggtgt 660
197 cattcccatt gggatgccgt ctggaagctc tacaaccaca ggactcaaat gggacctcaa 720

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198      tgatgcagcg atgagttttg gaggtttaat aagcacatca aatattgtaa aaggggaaat 780
199      agttacagta cagtctgatt cagatcttct ttggactatt tctattaaga agctctagga 840
200      ttacatggtt gcacagtgcc gtgatttttc agatctttga taccaattta tatgggtctt 900
201      gtccatitta aaggccagag cttctgctga cctttcttta tgtttcattc tttcaattta 960
202      ctctgtgaat tgtgggaggg tggaaaggaa ttagggaggtt attctttaat ataggaaggtt 1020
203      cagttttcaa agaggttact tacattcctt ggatcagttg cattgtatgt tattgttatc 1080
204      cgtaaagtga atagcagaat aagatggcaa aaaacaaaaa cagaaattta aagaaggaga 1140
205      aaatcatgtc atgtactatt ttgcttatgc atacagagca atggactgtt agttgccgct 1200
206      ctactctgtg gttcgggacc attaccacaa caggtcaatt attctgggta atttctatgt 1260
207      gataggggat tttcaattta gaagaatgag aaattattat gtgtgagacg ggctttgtaa 1320
208      ttacaagaa cgagttaata aaattttatt atgcatgagt ttgaatgcaa aaaaaaaaaa 1380
209      aaaaaaaaaa aaaaaaaaaa aaaaaa 1406
211 <210> SEQ ID NO: 8
212 <211> LENGTH: 259
213 <212> TYPE: PRT
214 <213> ORGANISM: Glycine max
215 <400> SEQUENCE: 8
216      Met Glu Leu Met Cys His Cys Ser Ser Phe Leu Leu Pro Pro Glu Asn
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218      Pro Asn Thr Thr Cys Ser Leu Ser Leu Lys Tyr Ala Leu Val Val Leu
219           20             25             30
220      Asn Gln Ser Leu Pro Arg Phe Ala Pro Leu Leu Trp Asp His Ala Gln
221           35             40             45
222      Val Arg Val Cys Ala Asp Gly Ala Asn Arg Val Tyr Asp Glu Met
223           50             55             60
224      Pro Leu Phe Phe Pro His Gln Gln Pro Ser His Val Arg Thr Arg Tyr
225           65             70             75             80
226      Lys Pro Asp Val Ile Lys Gly Asp Met Asp Ser Ile Arg Thr Glu Val
227           85             90             95
228      Leu Asp Phe Tyr Ala Lys Leu Gly Thr Lys Ile Ile Asp Glu Ser His
229           100            105            110
230      Asp Gln Asp Thr Thr Asp Leu His Lys Cys Val Ala Tyr Ile Arg Asp
231           115            120            125
232      Leu Thr Pro Asn Ile Asp Gly Ala Glu Leu Cys Ile Leu Val Ala Gly
233           130            135            140
234      Ala Leu Gly Gly Arg Phe Asp His Glu Ile Gly Asn Ile Asn Val Leu
235           145            150            155            160
236      Cys Arg Phe Ser Asn Thr Arg Ile Ile Leu Leu Ser Asp Asp Cys Leu
237           165            170            175
238      Ile His Leu Leu Pro Lys Asn His Cys His Lys Ile Phe Val Gln Ser
239           180            185            190
240      Ser Val Glu Gly Pro His Cys Gly Val Ile Pro Ile Gly Met Pro Ser
241           195            200            205
242      Gly Ser Ser Thr Thr Thr Gly Leu Lys Trp Asp Leu Asn Asp Ala Ala
243           210            215            220
244      Met Ser Phe Gly Gly Leu Ile Ser Thr Ser Asn Ile Val Lys Gly Glu
245           225            230            235            240
246      Ile Val Thr Val Gln Ser Asp Ser Asp Leu Leu Trp Thr Ile Ser Ile
247           245            250            255

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## VERIFICATION SUMMARY

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